What is claimed is:

1. A method for detection of mutations in the *pol* gene of HIV-1 isolates comprising the steps of:

a) isolation of a sample comprising HIV-1 RNA,

b) PCR amplifying RNA from said sample using a primer chosen from an outer primer as represented in SEQ ID No: 1 and 2 to obtain a primary PCR product,

c) PCR amplifying said primary PCR product using a 5' and 3' primer chosen from an inner primer as represented in SEQ ID No: 3, 4, 5 and 6 to obtain a secondary PCR product, and

d) sequencing said secondary PCR product.

2. A method according to Claim 1, wherein said secondary PCR product is sequenced using at least one sequencing primer chosen from primers as represented in SEQ ID No: 7 to 12.

3. A method according to Claim 1, wherein said RNA is viron RNA extracted from said sample.

4. A method according to Claim 2, wherein at least one of said sequencing primer is replaced by one or a pair of replacement primers.

5. A method according to Claim 1, wherein said secondary PCR product is sequenced using at least one sequencing primer chosen from primers up to 1, 2, 3 or 4 nucleotides upstream or downstream primer regions as represented in SEQ ID No: 7 to 12.

6. A method according to Claim 1, wherein the outer primer is chosen from primers up to 1, 2, 3 or 4 nucleotides upstream or downstream primer regions as represented in SEQ ID No: 1 and 2.

7. A method according to Claim 1, wherein the inner primer is chosen from primers up to 1, 2, 3 or 4 nucleotides upstream or downstream primer regions as represented in SEQ ID No: 3, 4, 5 and 6.

8. A method according to Claim 1, wherein the sample contains free virion particles or virus infected cells.

~~9. A method according to Claims 1, wherein said primary PCR product is sequenced using at least one sequencing primer chosen from any of SEQ ID No: 7 to 12.~~

10. A method for detection of mutations of the *pol* gene of HIV-1 isolates comprising the steps of:

a) isolation of a sample comprising HIV-1 DNA

b) PCR amplifying DNA from said sample using a primer chosen from outer primers as represented in SEQ ID No: 1 and 2 to obtain a primary PCR product,

d) PCR amplifying said primary PCR product using a 5' and 3' primer chosen from an inner primer as represented in SEQ ID No: 3, 4, 5 and 6 to obtain a secondary PCR product, and

e) sequencing this secondary PCR product.

11. A method according to Claim 10, wherein said secondary PCR product is sequenced using at least one sequencing primer chosen from primers as represented in SEQ ID No: 7 to 12.

12. A method according to Claim 10, wherein said DNA is viral DNA extracted from said sample.

13. A method according to Claim 11, wherein at least one of said at least one sequencing primer is replaced by one or a pair of replacement primers.

14. A method according to Claim 11, wherein said secondary PCR product is sequenced using at least one sequencing primer chosen from primers up to 1, 2, 3 or 4 nucleotides upstream or downstream primer regions as represented in SEQ ID No: 7 to 12.

15. A method according to Claim 10, wherein the outer primer is chosen up to 1, 2, 3 or 4 nucleotides upstream or downstream primer regions as represented in SEQ ID No: 1 and 2.

16. A method according to Claim 10, wherein the inner primer is chosen up to 1, 2, 3 or 4 nucleotides upstream or downstream primer regions as represented in SEQ ID No: 3, 4, 5 and 6.

17. A method according to Claim 10, wherein the sample contains free virion particles or virus infected cells.

18. A method according to Claims 10, wherein said primary PCR product is sequenced using at least one sequencing primer chosen from any of SEQ ID No: 7 to 12.

19. A primer for analyzing the sequence of the HIV *pol* gene of HIV-1 isolates chosen from the primers as represented in SEQ ID No: 1 and 5 to 12.

20. Diagnostic kit for the detection of mutations in the HIV *pol* gene of HIV-1 isolates comprising at least one of the primers having the sequence as represented in SEQ ID No: 1 to 12.

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